

RAW SEQUENCE LISTING

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Application Serial Number: 10/677, 983

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/677,983

DATE: 10/18/2004

TIME: 09:24:30

Input Set : N:\Crf3\RULE60\10677983.raw.txt

Output Set: N:\CRF4\10182004\J677983.raw

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1 <110> APPLICANT: FELDER, ROBIN A.
2   JOSE, PEDRO
3 <120> TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
4   HYPERTENSION
5 <130> FILE REFERENCE: FELDER 3.9-001 CONT
6 <140> CURRENT APPLICATION NUMBER: US/10/677,983
7 <141> CURRENT FILING DATE: 2003-10-02
8 <150> PRIOR APPLICATION NUMBER: US/09/614,748
9 <151> PRIOR FILING DATE: 2000-07-12
10 <150> PRIOR APPLICATION NUMBER: PCT/US99/00663
11 <151> PRIOR FILING DATE: 1999-01-12
12 <150> PRIOR APPLICATION NUMBER: 60/071,199
13 <151> PRIOR FILING DATE: 1998-01-12
14 <150> PRIOR APPLICATION NUMBER: 60/098,279
15 <151> PRIOR FILING DATE: 1998-08-28
16 <160> NUMBER OF SEQ ID NOS: 34
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 578
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
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27       20           25           30
28   Ile Leu Thr Leu Pro Pro Val Ser Gln Cys Ser Glu Leu Arg His Ser
29       35           40           45
30   Ile Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
31       50           55           60
32   Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Thr Leu Lys Arg His
33       65           70           75           80
34   Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
35       85           90           95
36   Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
37       100          105          110
38   Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu
39       115          120          125
40   Cys Arg Leu Gly Leu Lys Glu Glu Asn Pro Ser Lys Lys Ala Phe Glu
41       130          135          140
42   Glu Cys Thr Arg Val Ala His Asn Tyr Leu Arg Gly Glu Pro Phe Glu
43       145          150          155          160
44   Glu Tyr Gln Glu Ser Ser Tyr Phe Ser Gln Phe Leu Gln Trp Lys Trp

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45          165          170          175
46  Leu Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg His Tyr Arg Val
47          180          185          190
48  Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala
49          195          200          205
50  Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Gln Lys Lys Arg Ile Lys
51          210          215          220
52  Lys Arg Lys Gly Glu Ala Met Ala Leu Asn Glu Lys Arg Ile Leu Glu
53          225          230          235          240
54  Lys Val Gln Ser Arg Phe Val Val Ser Leu Ala Tyr Ala Tyr Glu Thr
55          245          250          255
56  Lys Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu
57          260          265          270
58  Lys Phe His Ile Tyr Asn Leu Gly Asn Pro Gly Phe Asp Glu Gln Arg
59          275          280          285
60  Ala Val Phe Tyr Ala Ala Glu Leu Cys Cys Gly Leu Glu Asp Leu Gln
61          290          295          300
62  Arg Glu Arg Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu
63          305          310          315          320
64  Asp Asp Arg Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Thr Glu
65          325          330          335
66  Ile Pro Glu Gly Gln Arg Val Arg Gly Arg Val Gly Thr Val Gly Tyr
67          340          345          350
68  Met Ala Pro Glu Val Val Asn Asn Glu Lys Tyr Thr Phe Ser Pro Asp
69          355          360          365
70  Trp Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Gln Gly His Ser
71          370          375          380
72  Pro Phe Lys Lys Tyr Lys Glu Lys Val Lys Trp Glu Glu Val Asp Gln
73          385          390          395          400
74  Arg Ile Lys Asn Asp Thr Glu Glu Tyr Ser Glu Lys Phe Ser Glu Asp
75          405          410          415
76  Ala Lys Ser Ile Cys Arg Met Leu Leu Thr Lys Asn Pro Ser Lys Arg
77          420          425          430
78  Leu Gly Cys Arg Gly Glu Gly Ala Ala Gly Val Lys Gln His Pro Val
79          435          440          445
80  Phe Lys Asp Ile Asn Phe Arg Arg Leu Glu Ala Asn Met Leu Glu Pro
81          450          455          460
82  Pro Phe Cys Pro Asp Pro His Ala Val Tyr Cys Lys Asp Val Leu Asp
83          465          470          475          480
84  Ile Glu Gln Phe Ser Ala Val Lys Gly Ile Tyr Leu Asp Thr Ala Asp
85          485          490          495
86  Glu Asp Phe Tyr Ala Arg Phe Ala Thr Gly Cys Val Ser Ile Pro Trp
87          500          505          510
88  Gln Asn Glu Met Ile Glu Ser Gly Cys Phe Lys Asp Ile Asn Lys Ser
89          515          520          525
90  Glu Ser Glu Glu Ala Leu Pro Leu Asp Leu Asp Lys Asn Ile His Thr
91          530          535          540
92  Pro Val Ser Arg Pro Asn Arg Gly Phe Phe Tyr Arg Leu Phe Arg Arg
93          545          550          555          560

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96      Gln Cys
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 546
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103      Met Glu Leu Glu Asn Ile Val Ala Asn Ser Leu Leu Leu Lys Ala Arg
104          1                      5                      10                      15
105      Gln Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
106                      20                      25                      30
107      Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Ile Leu Lys Arg His
108                      35                      40                      45
109      Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
110          50                      55                      60
111      Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
112          65                      70                      75                      80
113      Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu
114                      85                      90                      95
115      Cys Arg Leu Gly Leu Lys Glu Glu Asn Pro Ser Lys Lys Ala Phe Glu
116          100                      105                      110
117      Glu Cys Thr Arg Val Ala His Asn Tyr Leu Arg Gly Glu Pro Phe Glu
118          115                      120                      125
119      Glu Tyr Gln Glu Ser Ser Tyr Phe Ser Gln Phe Leu Gln Trp Lys Trp
120          130                      135                      140
121      Leu Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg His Tyr Arg Val
122          145                      150                      155                      160
123      Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala
124                      165                      170                      175
125      Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Gln Lys Lys Arg Ile Lys
126          180                      185                      190
127      Lys Arg Lys Gly Glu Ala Met Ala Leu Asn Glu Lys Arg Ile Leu Glu
128          195                      200                      205
129      Lys Val Gln Ser Arg Phe Val Val Ser Leu Ala Tyr Ala Tyr Glu Thr
130          210                      215                      220
131      Lys Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu
132          225                      230                      235                      240
133      Lys Phe His Ile Tyr Asn Leu Gly Asn Pro Gly Phe Asp Glu Gln Arg
134          245                      250                      255
135      Ala Val Phe Tyr Ala Ala Glu Leu Cys Cys Gly Leu Glu Asp Leu Gln
136          260                      265                      270
137      Arg Glu Arg Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu
138          275                      280                      285
139      Asp Asp Arg Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Thr Glu
140          290                      295                      300
141      Ile Pro Glu Gly Gln Arg Val Arg Gly Arg Val Gly Thr Val Gly Tyr
142          305                      310                      315                      320
143      Met Ala Pro Glu Val Val Asn Asn Glu Lys Tyr Thr Phe Ser Pro Asp

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144          325          330          335
145 Trp Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Gln Gly His Ser
146          340          345          350
147 Pro Phe Lys Lys Tyr Lys Glu Lys Val Lys Trp Glu Glu Val Asp Gln
148          355          360          365
149 Arg Ile Lys Asn Asp Thr Glu Glu Tyr Ser Glu Lys Phe Ser Glu Asp
150          370          375          380
151 Ala Lys Ser Ile Cys Arg Met Leu Leu Thr Lys Asn Pro Ser Lys Arg
152          385          390          395          400
153 Leu Gly Cys Arg Gly Glu Gly Ala Ala Gly Val Lys Gln His Pro Val
154          405          410          415
155 Phe Lys Asp Ile Asn Phe Arg Arg Leu Glu Ala Asn Met Leu Glu Pro
156          420          425          430
157 Pro Phe Cys Pro Asp Pro His Ala Val Tyr Cys Lys Asp Val Leu Asp
158          435          440          445
159 Ile Glu Gln Phe Ser Ala Val Lys Gly Ile Tyr Leu Asp Thr Ala Asp
160          450          455          460
161 Glu Asp Phe Tyr Ala Arg Phe Ala Thr Gly Cys Val Ser Ile Pro Trp
162          465          470          475          480
163 Gln Asn Glu Met Ile Glu Ser Gly Cys Phe Lys Asp Ile Asn Lys Ser
164          485          490          495
165 Glu Ser Glu Glu Ala Leu Pro Leu Asp Leu Asp Lys Asn Ile His Thr
166          500          505          510
167 Pro Val Ser Arg Pro Asn Arg Gly Phe Phe Tyr Arg Leu Phe Arg Arg
168          515          520          525
169 Gly Gly Cys Leu Thr Met Val Pro Ser Glu Lys Glu Val Glu Pro Lys
170          530          535          540
171 Gln Cys
172          545
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 532
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 3
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180 1 5 10 15
181 Gln Gly Gly Tyr Gly Lys Lys Ser Gly Arg Ser Lys Lys Trp Lys Glu
182 20 25 30
183 Ile Leu Thr Leu Pro Pro Val Ser Gln Cys Ser Glu Leu Arg His Ser
184 35 40 45
185 Ile Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
186 50 55 60
187 Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Ile Leu Lys Arg His
188 65 70 75 80
189 Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
190 85 90 95
191 Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
192 100 105 110
193 Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu

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194																
195	Cys	Arg	Leu	Gly	Leu	Lys	Glu	Glu	Asn	Pro	Ser	Lys	Lys	Ala	Phe	Glu
196			130					135					140			
197	Glu	Cys	Thr	Arg	Val	Ala	His	Asn	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	Glu
198							150					155				160
199	Glu	Tyr	Gln	Glu	Ser	Ser	Tyr	Phe	Ser	Gln	Phe	Leu	Gln	Trp	Lys	Trp
200						165					170					175
201	Leu	Glu	Arg	Gln	Pro	Val	Ile	Lys	Asn	Thr	Phe	Arg	His	Tyr	Arg	Val
202						180				185					190	
203	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala
204						195			200				205			
205	Thr	Gly	Lys	Met	Tyr	Ala	Cys	Lys	Lys	Leu	Gln	Lys	Lys	Arg	Ile	Lys
206			210					215					220			
207	Lys	Arg	Lys	Gly	Glu	Ala	Met	Ala	Leu	Asn	Glu	Lys	Arg	Ile	Leu	Glu
208							230					235				240
209	Lys	Val	Gln	Ser	Arg	Phe	Val	Val	Ser	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr
210						245					250					255
211	Lys	Asp	Ala	Leu	Cys	Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu
212						260				265					270	
213	Lys	Phe	His	Ile	Tyr	Asn	Leu	Gly	Asn	Pro	Gly	Phe	Asp	Glu	Gln	Arg
214						275				280				285		
215	Ala	Val	Phe	Tyr	Ala	Ala	Glu	Leu	Cys	Cys	Gly	Leu	Glu	Asp	Leu	Gln
216						290			295				300			
217	Arg	Glu	Arg	Ile	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu
218							310					315				320
219	Asp	Asp	Arg	Gly	His	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Thr	Glu
220						325					330					335
221	Ile	Pro	Glu	Gly	Gln	Arg	Val	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr
222						340				345					350	
223	Met	Ala	Pro	Glu	Val	Val	Asn	Asn	Glu	Lys	Tyr	Thr	Phe	Ser	Pro	Asp
224						355			360					365		
225	Trp	Trp	Gly	Leu	Gly	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Gln	Gly	His	Ser
226							370						380			
227	Pro	Phe	Lys	Lys	Tyr	Lys	Glu	Lys	Val	Lys	Trp	Glu	Glu	Val	Asp	Gln
228							385					390				400
229	Arg	Ile	Lys	Asn	Asp	Thr	Glu	Glu	Tyr	Ser	Glu	Lys	Phe	Ser	Glu	Asp
230						405					410					415
231	Ala	Lys	Ser	Ile	Cys	Arg	Met	Leu	Leu	Thr	Lys	Asn	Pro	Ser	Lys	Arg
232						420				425					430	
233	Leu	Gly	Cys	Arg	Gly	Glu	Gly	Ala	Ala	Gly	Val	Lys	Gln	His	Pro	Val
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/677,983

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